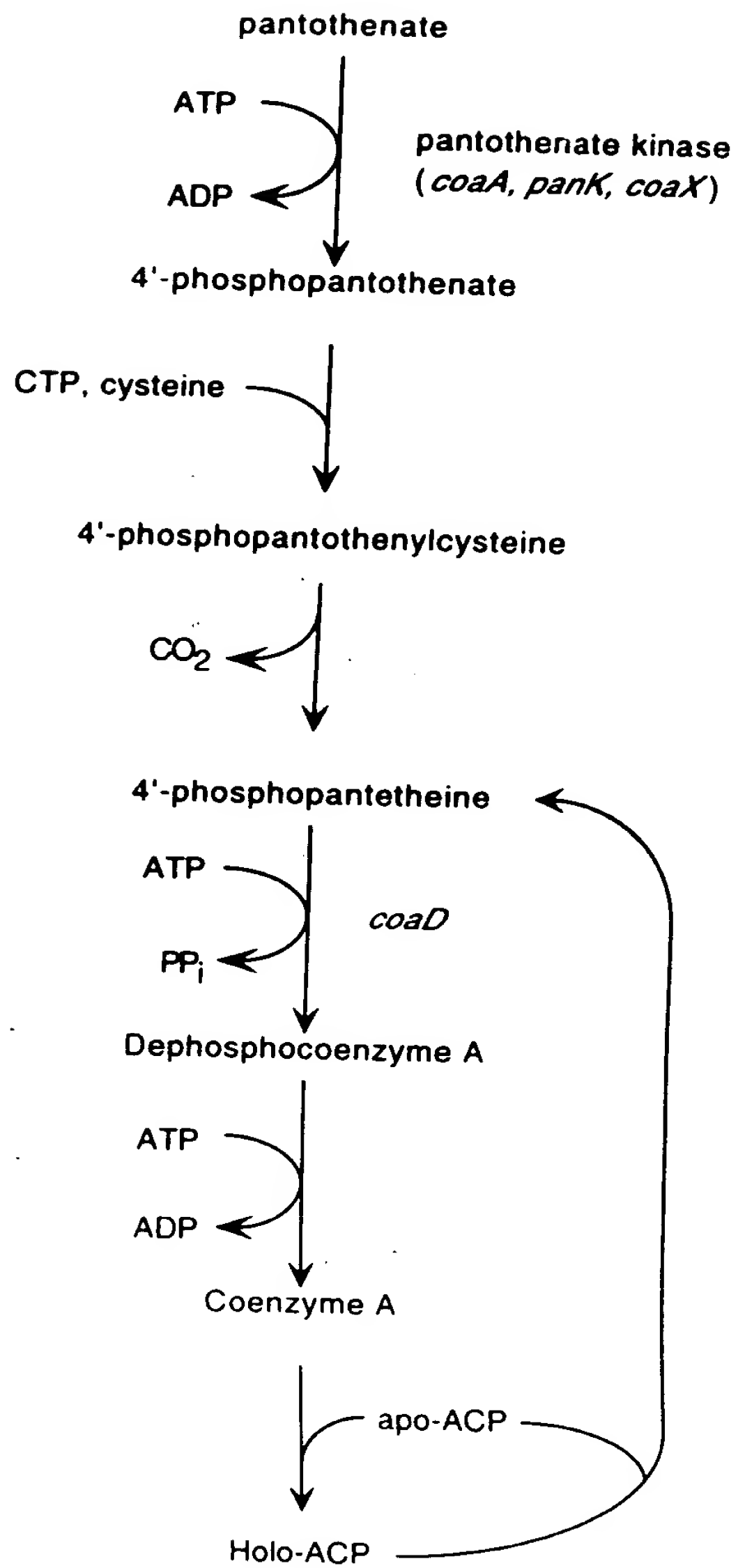
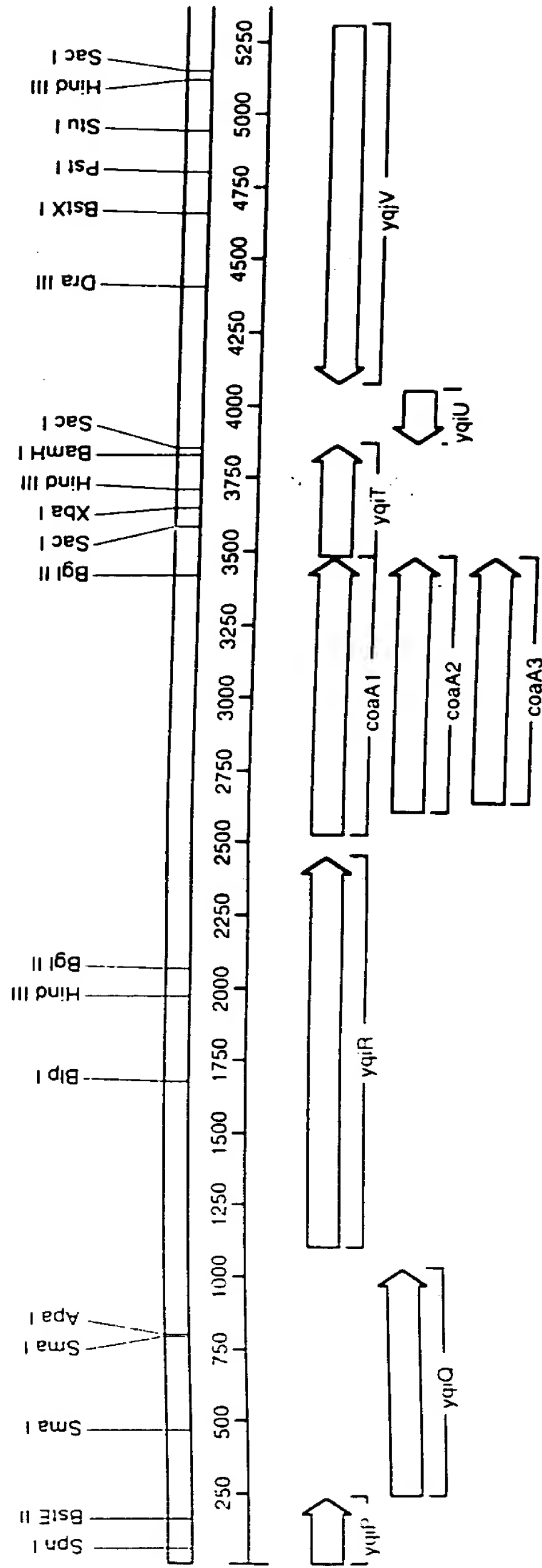


Figure 267

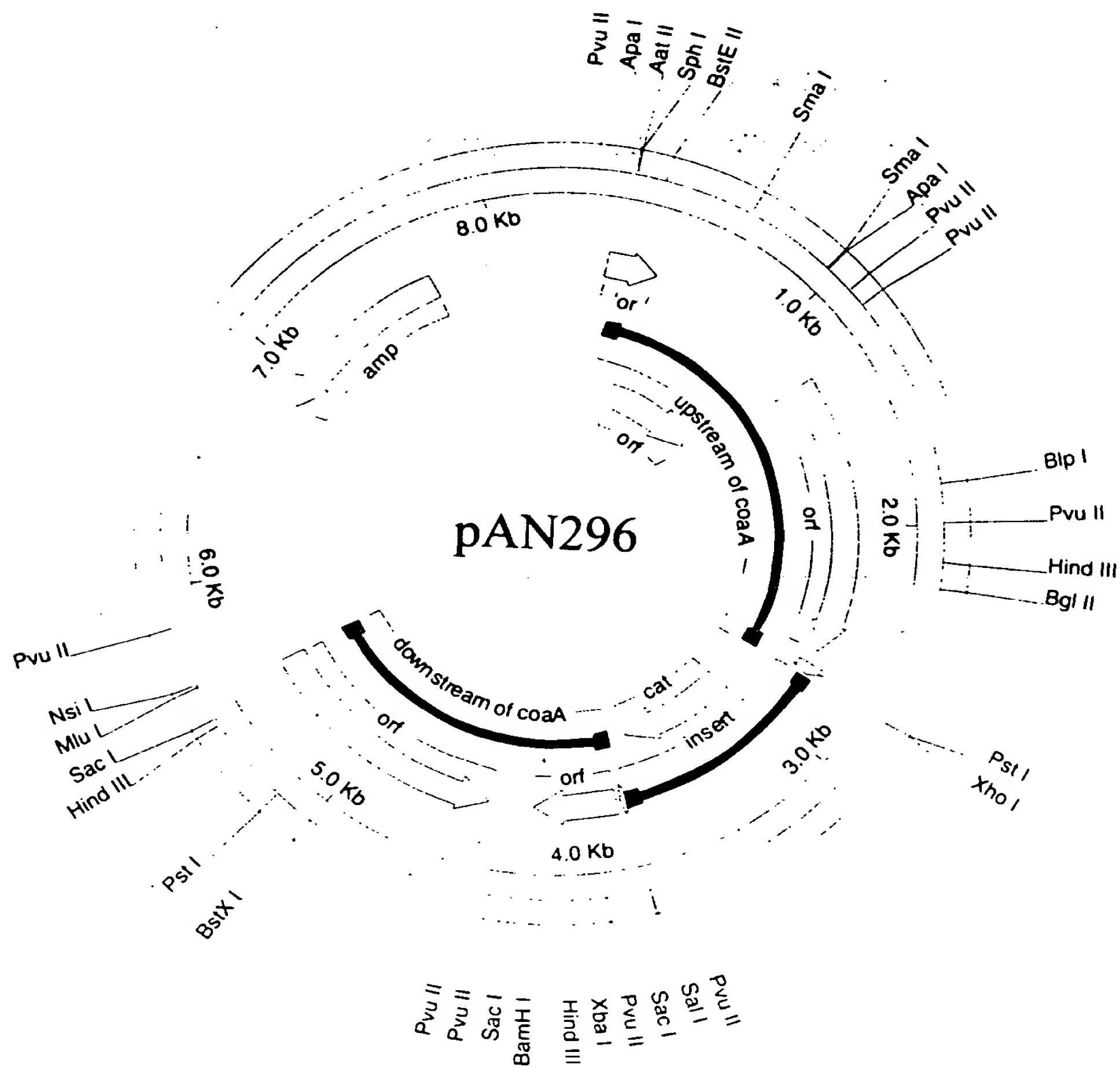


2

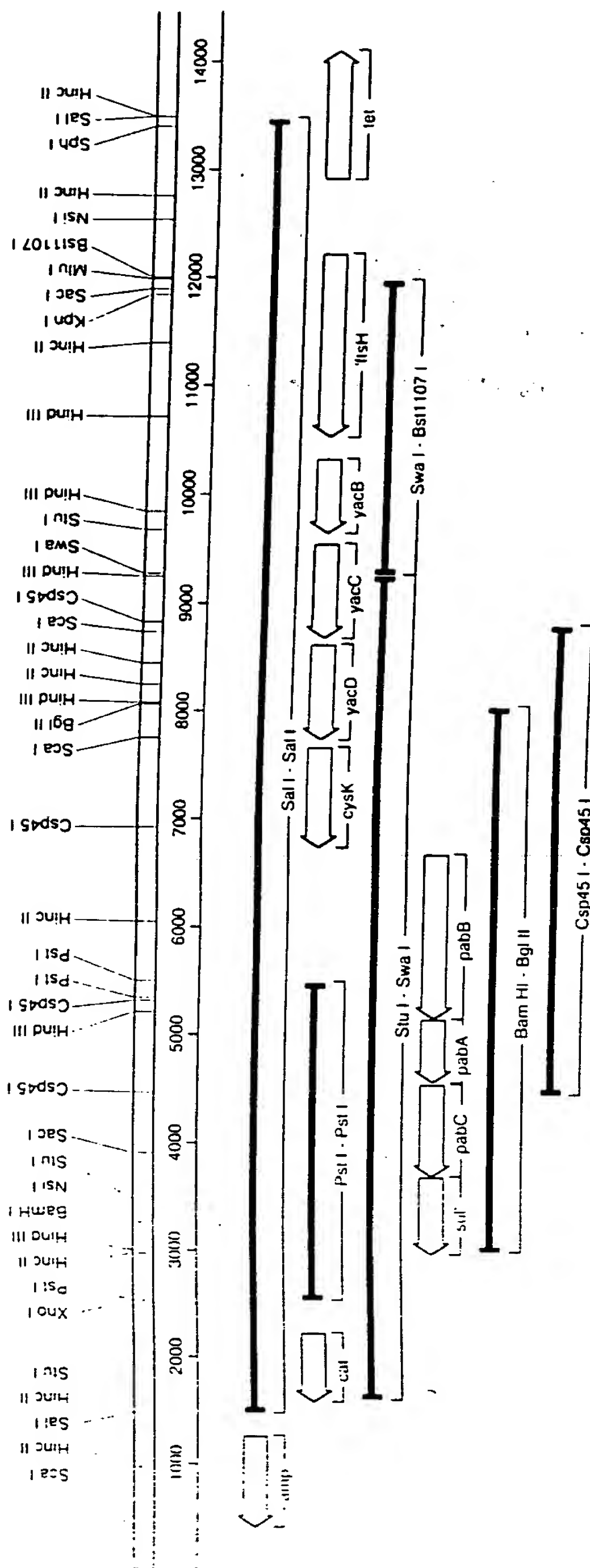
Figure 18 Structure of the *B. subtilis* chromosome in the region of the *coaA* gene. The scale is in base pairs and the significant open reading frames are shown by the open arrows.



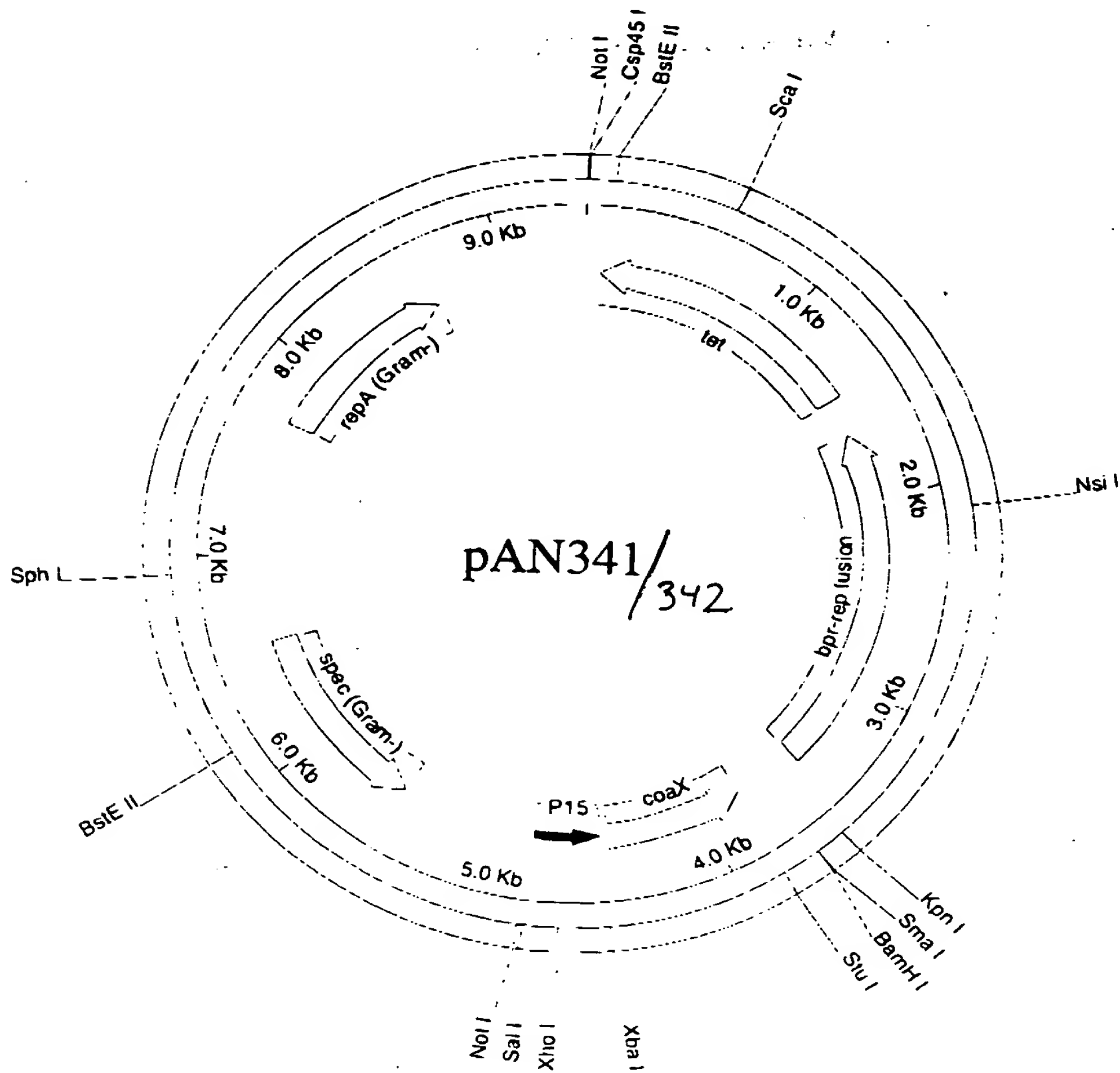
13
 Figure 1 Structure of pAN296, designed to delete most of the *B. subtilis* *coaA* gene and substitute a chloramphenicol resistance gene.



4
Figure 21



5
Figure 27 Structure of pAN341 and pAN342, two independent PCR-derived clones of *yacB* (renamed *coaX*).



6A

FIG. 28A

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence type explicitly set to Protein

Sequence format is Pearson

Seq. 1:	B.subtilis Coax SEQNO. 2	258 aa	Seq. 8:	sp O51477 B.burgdorferi	262 aa
Seq. 2:	dbj BAA21476.1 D.vulgaris	212 aa	Seq. 9:	sp P74045 Synechocystis	257 aa
Seq. 3:	gb AAD35964.1 T.maritima	246 aa	Seq. 10:	sp O25533 H.pylori	223 aa
Seq. 4:	pir T36391 S.coelicolor	265 aa	Seq. 11:	sp O67753 A.aeolicus	229 aa
Seq. 5:	sp Q45338 B.pertussis	267 aa	Seq. 12:	sp Q9RX54 D.radiodurans	262 aa
Seq. 6:	sp O06282 M.tuberculosis	272 aa	Seq. 13:	WIT RCA03301 C.acetobutylicum	250 aa
Seq. 7:	sp O83446 T.pallidum	273 aa	Seq. 14:	WIT RRC02473 R.capsulatus	258 aa

B.subtilis|Coax|SEQIDNO. 2
WIT|RCA03301|C.acetobutylicum
pir|T36391|S.coelicolor
sp|O06282|M.tuberculosis
WIT|RRC02473|R.capsulatus
dbj|BAA21476.1|D.vulgaris
sp|Q9RX54|D.radiodurans
gb|AAD35964.1|T.maritima
sp|O83446|T.pallidum
sp|O51477|B.burgdorferi
sp|O67753|A.aeolicus
sp|P74045|Synechocystis
sp|O25533|H.pylori
sp|Q45338|B.pertussis

-----MLLVIDVGNTNTVLGVYHDG-----KLEYHWRIE
NKRAAFMLLLFLRSVLKVILVLDVGNTNIVLGIYNDT-----KLTAEWRLS
-----MLLTIDVGNTHTVLGLFDGE-----DIVEHWRIS
-----MLLAIDVRNTHTVVGLLSGMKEHAKVVQQWRIR
-----MLLCIDCGNTNTVFSVWDGT-----DFAATWRIA
-----MTQHFLFLFDIGNTNVKGIAVET-----AVLTSYVLP
-----MPAFPLLAVIDIGNTTTVLGLADASG-----ALHTWRIIR
-----MYLLVDVGNTHSVFSITEDG-----KTFRRWRLS
-----MLLIDVGNSHVFGIQGENGGRVCVRELFRLA
-----MNKPLLSELIIDIGNTSIAFALFKDN-----QVNLFIKMK
-----MRFLTVDVGNSSDIALWEGK-----KVK
-----METSKEGGLALDNDKQKPLWGLMIGN-----SRLHWAYC
-----MPARQSFTDLKN-----LVLCDIGN-----TR
-----MIILIDSGNSRLKVGWFDPDAP--QAAREPAPV
* :

2
B. subtilis|Coax|SEQIDNO_2
WIT|RCA03301|C.acetobutylicum
pir|T36391|S.coelicolor
sp|O06282|M.tuberculosis
WIT|RRC02473|R.capsulatus
dbj|BAA21476.1|D.vulgaris
sp|Q9RX54|D.radiodurans
gb|AAD35964.1|T.maritima
sp|O83446|T.pallidum
sp|O51477|B.burgdorferi
sp|O67753|A.aeolicus
sp|P74045|Synechocystis
sp|O25533|H.pylori
sp|Q45338|B.pertussis

2
B. subtilis|Coax|SEQIDNO_2
WIT|RCA03301|C.acetobutylicum
pir|T36391|S.coelicolor
sp|O06282|M.tuberculosis
WIT|RRC02473|R.capsulatus
dbj|BAA21476.1|D.vulgaris
sp|Q9RX54|D.radiodurans
gb|AAD35964.1|T.maritima
sp|O83446|T.pallidum
sp|O51477|B.burgdorferi
sp|O67753|A.aeolicus
sp|P74045|Synechocystis
sp|O25533|H.pylori
sp|Q45338|B.pertussis

TSRHKTEDEFGMILRSLFDHS-----GLMFEQIDGIIISSVVPIMPALER
TDVLRSADEYGIQVMNLFQD-----KLDPTLVEGVIISSVVPNIMYSLEH
TDSRRTADELAVLLQGLMGHPLLGLDELGDGIDGIAICATVPSVLHELRE
TESEVTADELALTIDGLIG-----EDSERLTGTAALSTVPSVLHEVRI
TDHRRTADEYFVWNLTMQLK-----GLQGRISEAIISSSTAPRWVFNLRV
TDPGQTTDSIGLRLLLEVLRHAG-----LGPADVGCACVSSWPGVWNLIRR
TNREMLPDDLALQLHGLFTLA-----GAP-IPRAAVLSSVAPPVGENYAL
TGVFQTEDELFSHLHPLLG-----DAMREIKGIGVASWVPTQNTVIER
PDARKTQDEYSLLIHALCERAG-----VGRASLRDAFISSWVPVLTKTIA
TNLMRLRYDEVYSFFEENFDN-----VN--K-VFISSVWPILNETFKN
DFLKLSSHEEFKEEFPKLK-----ALGISVKQSFSEKVRG
SGNAPLQTVWTDYNPKSAQLP-----VLLGKVPLMLASVWPE
IHFAQNYQLFSSAKEDLKR-----LGIQKEIFYISVNEE
AFDNLDLDALGRWLATLPRRP-----Q-----RALGVNVAGLARGEAIA

MCTKYFHIQPIVG-PG-MKTGLNINIKYDNPKEVGADRIVNAVAIHLYG-
MIRKYFKINPLVVG-PG-IKTGINIKYDNPKEVGADRIVNAVAHEIYK-
VTRRYYGDVPAVLVEPG-VKTGVPIILTDHPKEVGADRIINAVAARELYG-
MLDQYWPSPVPHVLIIEPG-VRTGIPLLVDPNPKEVGADRIINCLAAAYDRFR-
LCNRYFDCRPYVVGKPG-CELPVAPRVDPGTTVGPDLRVNTVAGYDRHG-
ACERYL--YRKLFPAGDIAIPLDNRVERPAEVEVGADRLVAAAYARRLYP-
ALKRHFMDAFVSAEN--LPDVTVELDTPGSVGADRLCNLFGAEKYL-
FSQYFHIPIWVKAEN--GCVMNVKNPSEVGADRVANVAVFVKEYG-
AVAQISGVQPVWFGPWAYEHLPVRIPEPVRAEIGTDLVANAVAAVYHFR-
VIFSFFKIKPLFIGFDLNYDLTFNPYKSDKELLGSDVFANLVAAIENYS-
KIPKIK-----FLKKEN--FPIQVDYKTPETLGTDRVALAYSAKKFGY-
QTEVWRVYQPKILTAKN--LPLVNLYP---SFGIDRALAGLGTGLTYG-
NEKALLNCYPNAKNIAG--FFHLETDYVG---LGIDRQMACLA---VN--
ATLRAGGCDIRWLRQP-LAMGLRNGYRNPDLQGLADRWACMVGLARQPS

6B
FIG.23B

2

2.

• •
• •
• •
• •
• •

•

62

2
B. subtilis|Coax|SEQIDNO 5
WIT|RCA03301|C.acetobutylicum
pir|T36391|S.coelicolor
sp|O06282|M.tuberculosis
WIT|RRC02473|R.capsulatus
dbj|BAA21476.1|D.vulgaris
sp|Q9RX54|D.radiodurans
gb|AAD35964.1|T.maritima
sp|O83446|T.pallidum
sp|O51477|B.burgdorferi
sp|O67753|A.aeolicus
sp|P74045|Synechocystis
sp|Q25533|H.pylori
sp|Q45338|B.pertussis

2
B. subtilis|Coax|SEQIDNO 5
WIT|RCA03301|C.acetobutylicum
pir|T36391|S.coelicolor
sp|O06282|M.tuberculosis
WIT|RRC02473|R.capsulatus
dbj|BAA21476.1|D.vulgaris
sp|Q9RX54|D.radiodurans
gb|AAD35964.1|T.maritima
sp|O83446|T.pallidum
sp|O51477|B.burgdorferi
sp|O67753|A.aeolicus
sp|P74045|Synechocystis
sp|Q25533|H.pylori
sp|Q45338|B.pertussis

60
FIG. 23D

-----VIATGG-----LAPLIANES-----DCIDIVDPFLLTKGLELI
RTSLVLATGG-----LAKLIN-----
DDVTVIATGG-----LAPMVLGES-----SVIDEHEPWLTLMGLRLV
HDVAIVATGH-----TAPLLLPPEL-----HTVDHYDQHLTLQGLRLV
--MKVIATGG-----LASLFDLGF-----DLFDKVEDDLTMHGLRLI

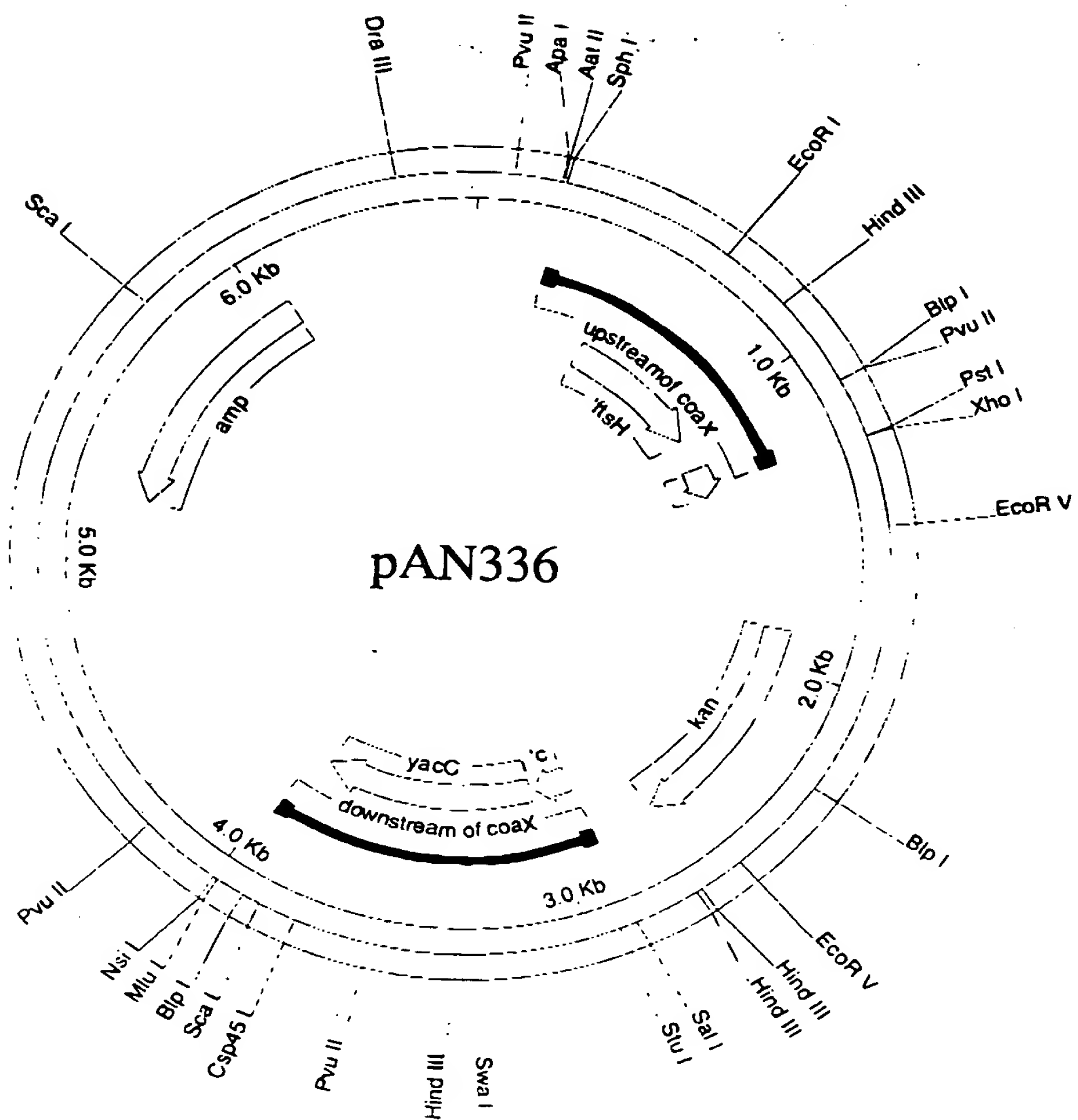
--AVAVATGG-----FSRTVQGIC-----QEIDYYDETTLRGLVEL
-----VVLTTGG-----QSKIVK-DM-----IKHEIFDEDLTIKGVYHF
--CAAVITGG-----LSRLFS-SE-----VDFPPIDAQLTSLGLAHI
--FNLIITGG-----NADLILSLI-----EIEFIFNIHLTVEGVRIL
--FKVVTGG-----EGKYFS-----KFGIYDPLLVRGMRNL
--AMVITGG-----DGKILHGFLKEHSPNLSVAWDDNLIIFLGMAAI
-----IYLCGG-----DAKYLSAFL-----PHSVCKERLVFDGMEIA
--EIVVAGGWNPEVRQEAERLLAVTGAAFGATPQPTYLDSPVLDGLAAL

YERNRVGSV-----

YERNVSRM-----
FERNLEVQRGLKTAR-----
FDYNKGLGA-----

WASRSEVR-----
CFGD-----
ARLVPTSLPPATVSGSSGN
GNSIDFKFVN-----
LYLYHRI-----
HHGDRPIC-----
LKKAGILECK-----
AAQGAPTA-----

Figure 2 Structure of pAN336, a plasmid designed to delete *B. subtilis* *coaX* from the chromosome and replace it with a kanamycin resistance gene.



Construction of pOTP72

Fig 8

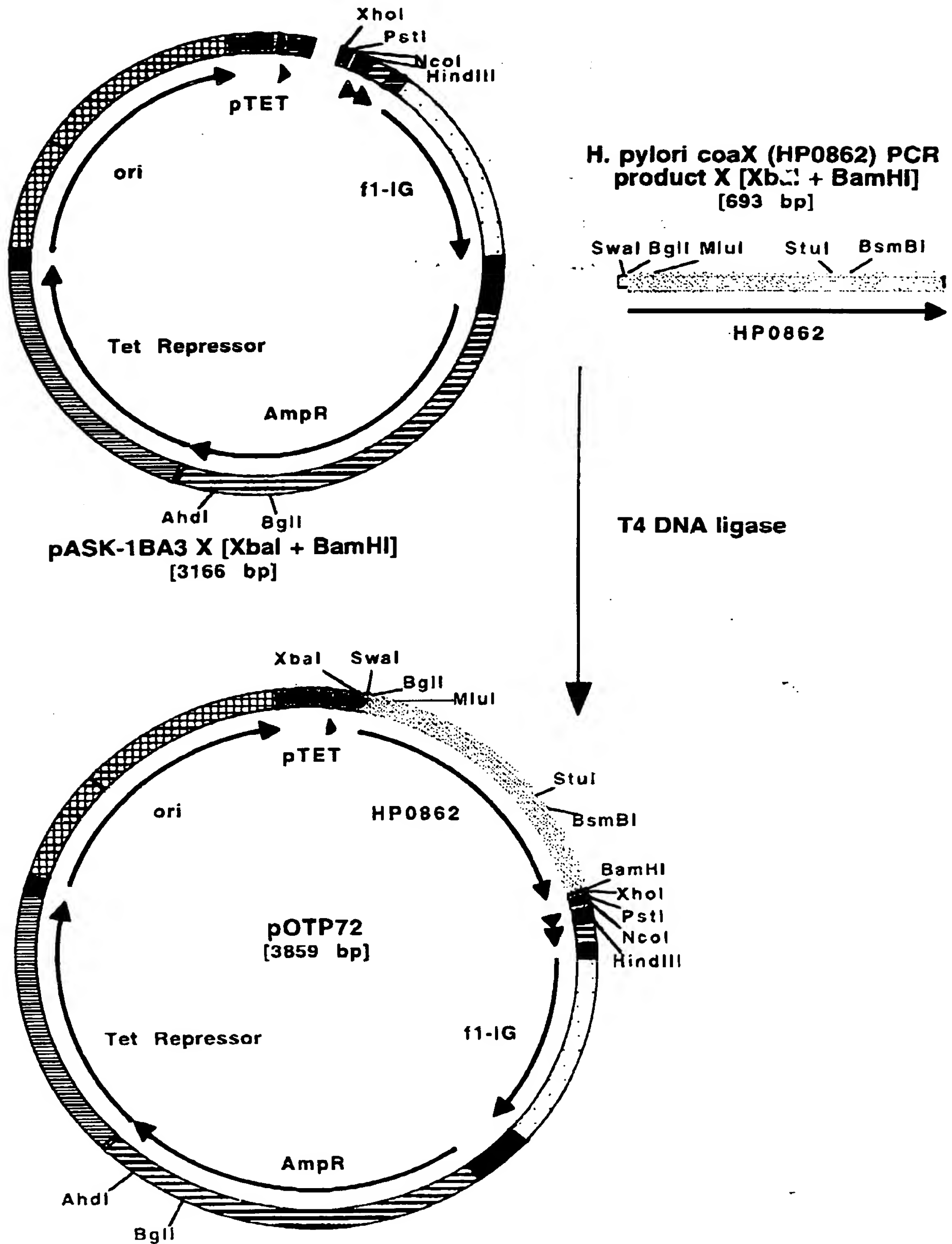


Fig 9

Construction of pOTP73

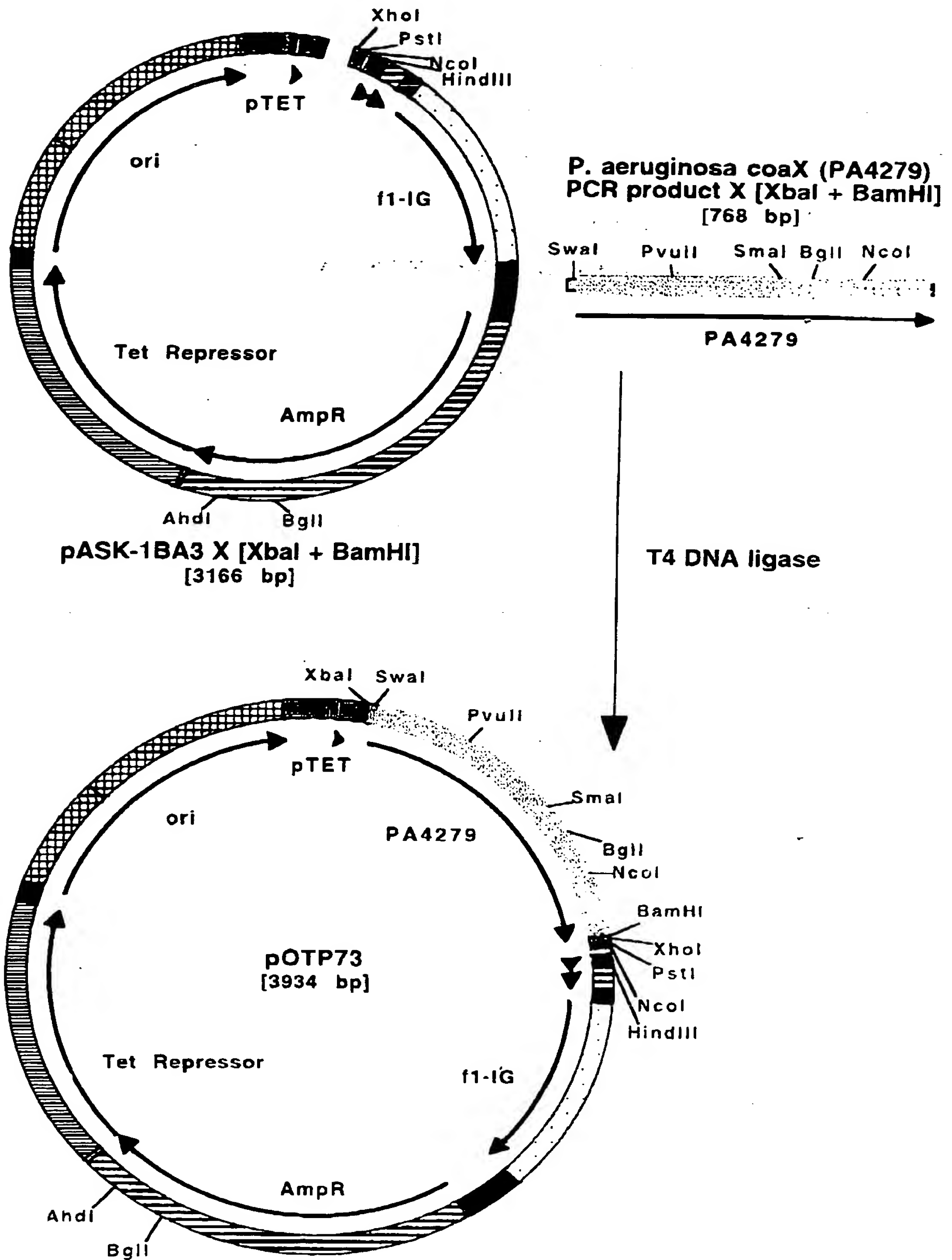


Fig 10

Construction of pOTP71

